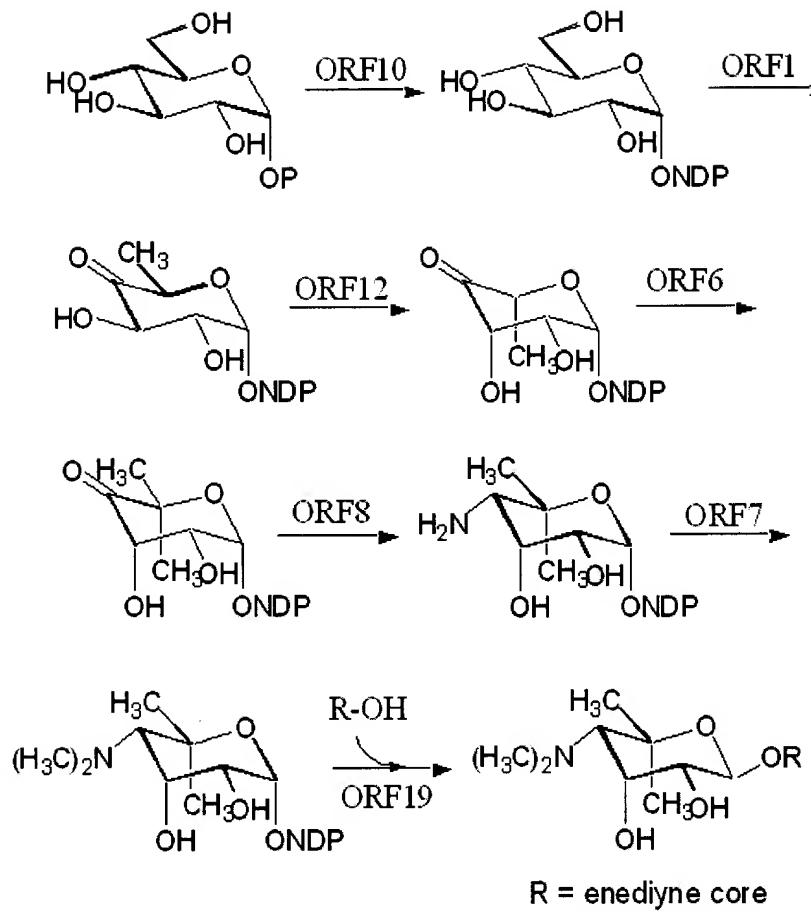


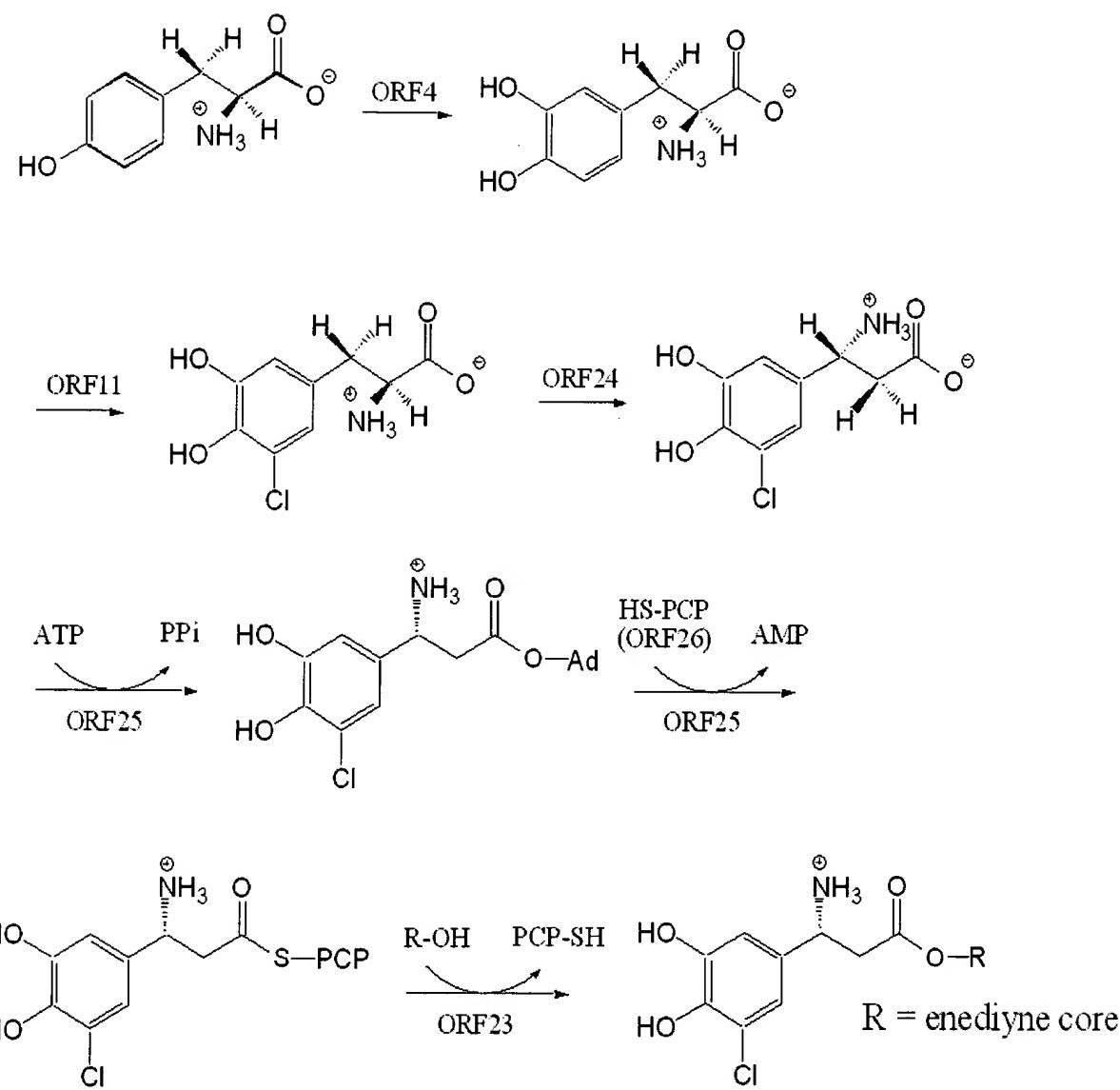
Fig. 1



ORF10: dNDP-glucose synthase, 355 aa
 ORF1: dNDP-glucose dehydratase, 332 aa
 ORF12: epimerase, 192 aa
 ORF8: aminotransferase, 410 aa

ORF6: C-methyltransferase, 423 aa
 ORF7: N-methyltransferase, 244 aa
 ORF19: glycosyl transferase, 459 aa

Fig. 2



ORF4: Hydroxylase, 527 aa

ORF11: Hydroxylase halogenase, 492/494 aa

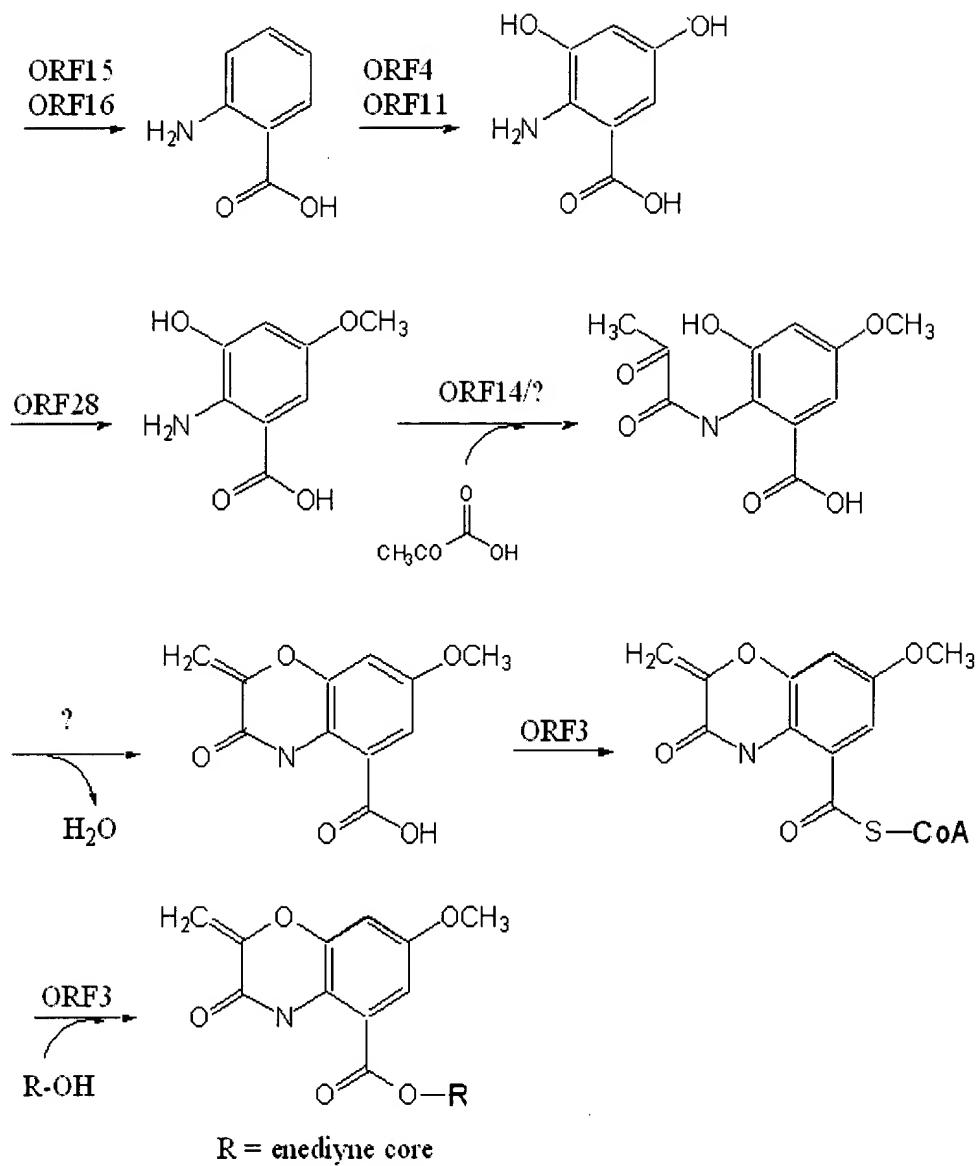
ORF24: Aminomutase, 539 aa

ORF23: Type II NRPS condensation enzyme, 459 aa

ORF25: Type II NRPS adenylation enzyme, 716 aa

ORF26: Type II peptidyl carrier protein 93 aa

Fig. 3A



ORF15: Anthranilate synthase I, 493 aa
ORF16: Anthranilate synthase II, 220 aa
ORF28: O-methyltransferase, 350 aa

ORF3: Coenzyme F390 synthetase, 463 aa
ORF14: Coenzyme F390 synthetase, 484 aa
ORF13: O-acyltransferase, 378 aa

Fig. 3B

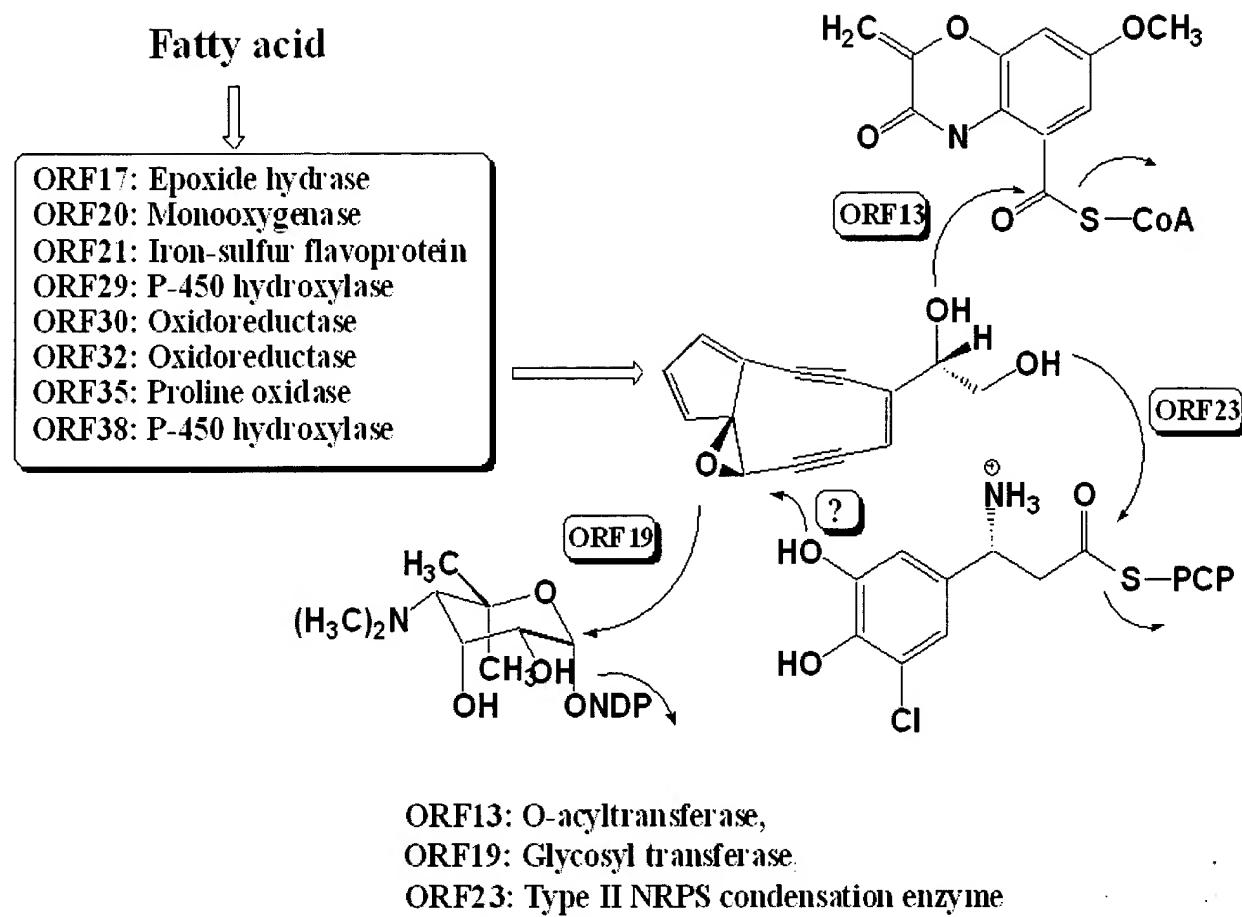


Fig. 4

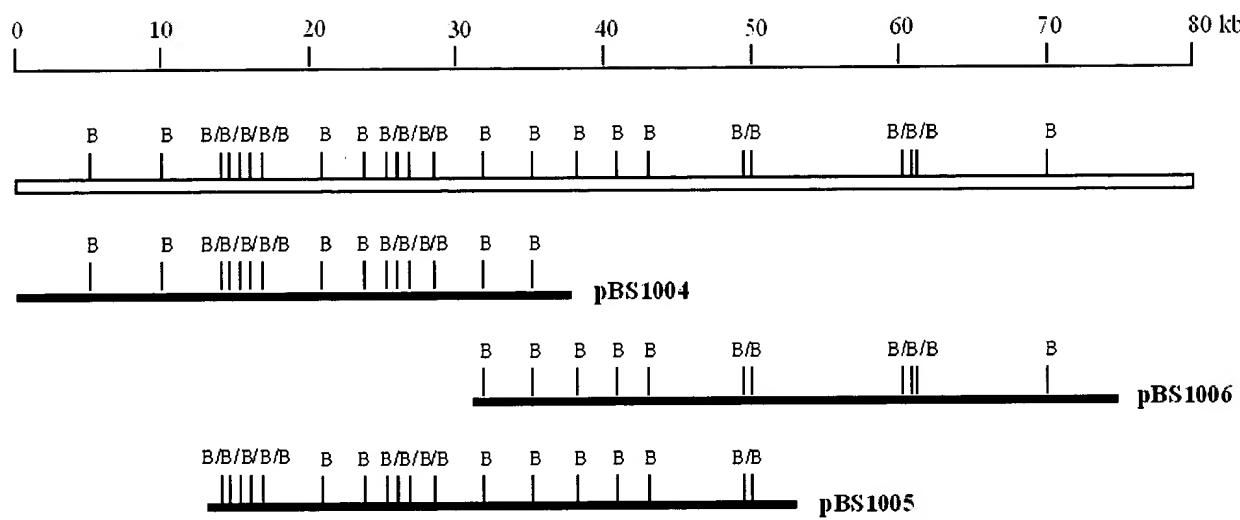


Fig. 5A

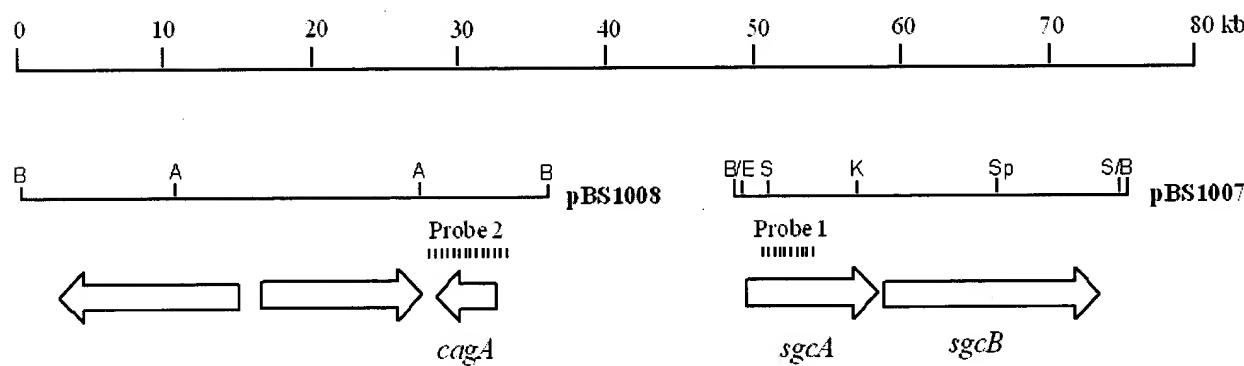


Fig. 5B

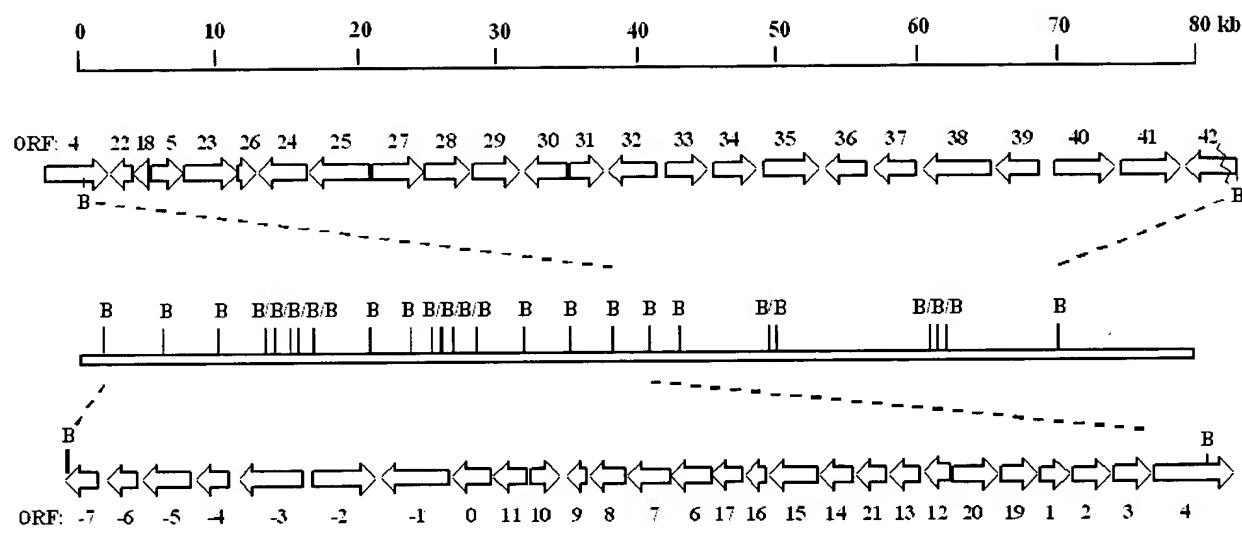


Fig. 5C



| | | |
|-----------|---|---|
| Gdh | 1:~~~ Ty1A2 | 1:~~~ MRVLTGGAGFIGSHYVROLIGGAYPAFAGADVVVLDKLYAGNEEENLRPVADDPRE: 57 |
| SgCA | 1:~~~ MRM | 1:~~~ MRVLTGGAGFIGSHYVROLIGGAYPDIGATRTVVLDKLYAGNPANLHVAGHPDL: 57 |
| MtmE | 1:MTTSI | 1:MTTSI LT VTGGAGFIGSHYVRLIGPR. GVPDVTVT LT DKLYAGTLTNLAEVSDSDRE: 58 |
| consensus | 1: mrvLTGGAGFIGShyvr | 1L g pa v VLDKLTYaGn NL va p r f: 60 |
| Gdh | 58:RFVRGDIICEWDVYSEVMREV | 58:RFVRGDIADHGWWRRILMEGVLVVHFAAE SHYDRSIE SSEA FVRNTVNE GTRVILQAAVDA: 117 |
| Ty1A2 | 58:EFVRGDIADHGWWRRILMEGVLVVHFAAE SHYDRSIE SSEA FVRNTVNE GTRVILQAAVDA: 117 | |
| SgCA | 58:TFVQGDTVDPRV | 58:TFVQGDTVDPRVDEVVAGHDVIVVHFAAE SHYDRSISDTATRFVTTNVLGTQVILDAALRH: 117 |
| MtmE | 59:RFVRGDI | 59:RFVRGDI |
| consensus | 61: FVrGDI d vv evm d vvvHFAAE s HVDRSI a | 59:CDAPL V DDLLAVHDQVHVFAAE SHYDRSISILGAADFVRNTVNE GTRVILQAAVDRQ: 118 FVrGDI d vv evm d vvvHFAAE s HVDRSI a FV TNV GTn tLL aA1 :120 |
| Gdh | 118:NVSKFVHVSTDEVYGGTIEHGSWPE | 118:NVSKFVHVSTDEVYGGTIEHGSWPE |
| Ty1A2 | 118:GVGREFVHISTDEVYGSIAEGSWPE | 118:GVGREFVHISTDEVYGSIAEGSWPE |
| SgCA | 118:GVGREFVHVSTDEVYGSIASGSWTE | 118:GVGREFVHVSTDEVYGSIASGSWTE |
| MtmE | 119:GIETEVHISTDEVYGSIDAGSWPE | 119:GIETEVHISTDEVYGSIDAGSWPE |
| consensus | 121:9v kFvHVSTDEVYGS1 GSWPEd p1 | 121:9v kFvHVSTDEVYGS1 GSWPEd p1 PNSPY A KAGSDLiAIAVHRTHGLdv vTR: 180 |
| Gdh | 178:CSNNYGPYQFPEKVLPFIFTNLMDGRRV | 178:CSNNYGPYQFPEKVLPFIFTNLMDGRRV |
| Ty1A2 | 178:CSNNYGPROYPEKAVPLFTNLMDGRRV | 178:CSNNYGPROYPEKAVPLFTNLMDGRRV |
| SgCA | 178:CSNNYGPYQYPEKVPLFVNTNLMDGRRV | 178:CSNNYGPYQYPEKVPLFVNTNLMDGRRV |
| MtmE | 179:CSNNYGSHQFPEKVPLFVTSLLDGR | 179:CSNNYGSHQFPEKVPLFVTSLLDGR |
| consensus | 181:CsNNYGp QFPEKVLPFIFTNLMDG RvLYGDG n RdWLHV DHCrgi 1V | 181:CsNNYGp QFPEKVLPFIFTNLMDG RvLYGDG n RdWLHV DHCrgi 1V GRaG: 240 |
| Gdh | 238:EIYNIGGGTELINKELTERVELM | 238:EIYNIGGGTELINKELTERVELM |
| Ty1A2 | 238:VIYNIGGGTELINKELTDRILEL | 238:VIYNIGGGTELINKELTDRILEL |
| SgCA | 238:EVYHIGGGTELNSNEELTGLLTA | 238:EVYHIGGGTELNSNEELTGLLTA |
| MtmE | 239:EVYHIGGGTELNSNEELTGLLTA | 239:EVYHIGGGTELNSNEELTGLLTA |
| consensus | 241:eiYnIGGGTELNT ELT vLe | 241:eiYnIGGGTELNT ELT vLe CG dws v V DR GHDRRYSvD TKir ELGY P :300 |
| Gdh | 298:VPEERGLAETIEWYRDNERAWWEPLKSAPDGGK~~~: 329 | 298:VPEERGLAETIEWYRDNERAWWEPLKSAPDGGK~~~: 329 |
| Ty1A2 | 298:TGITEGLAGTVAWYRDNERAWWEPLKRS | 298:TGITEGLAGTVAWYRDNERAWWEPLKRS |
| SgCA | 298:VAEEDGLAATV | 298:VAEEDGLAATV |
| MtmE | 299:REFGDALAE | 299:REFGDALAE |
| consensus | 301: F eglA T _v WYrdnRaWWWePLk a g | 301: F eglA T _v WYrdnRaWWWePLk a g : 336 |

Fig. 7

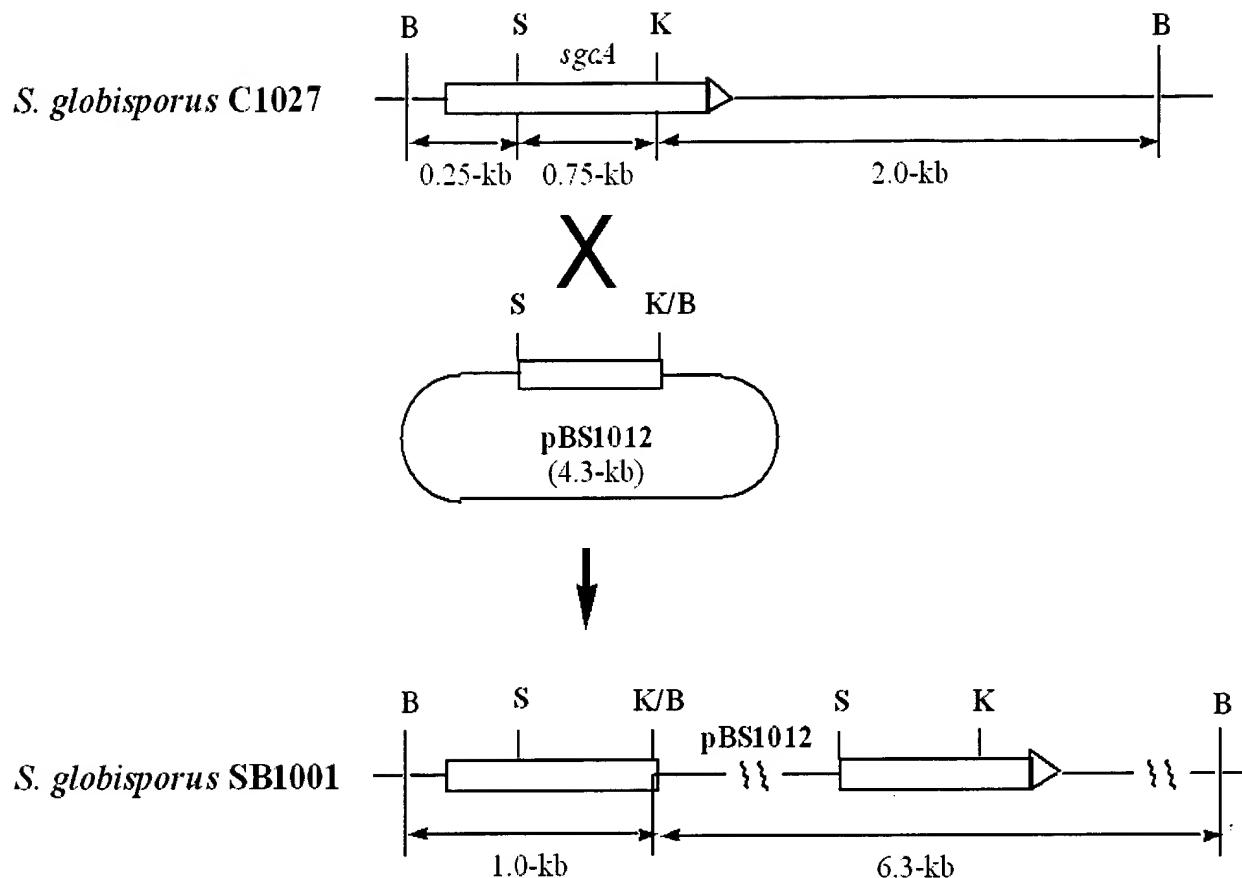


Fig. 8A

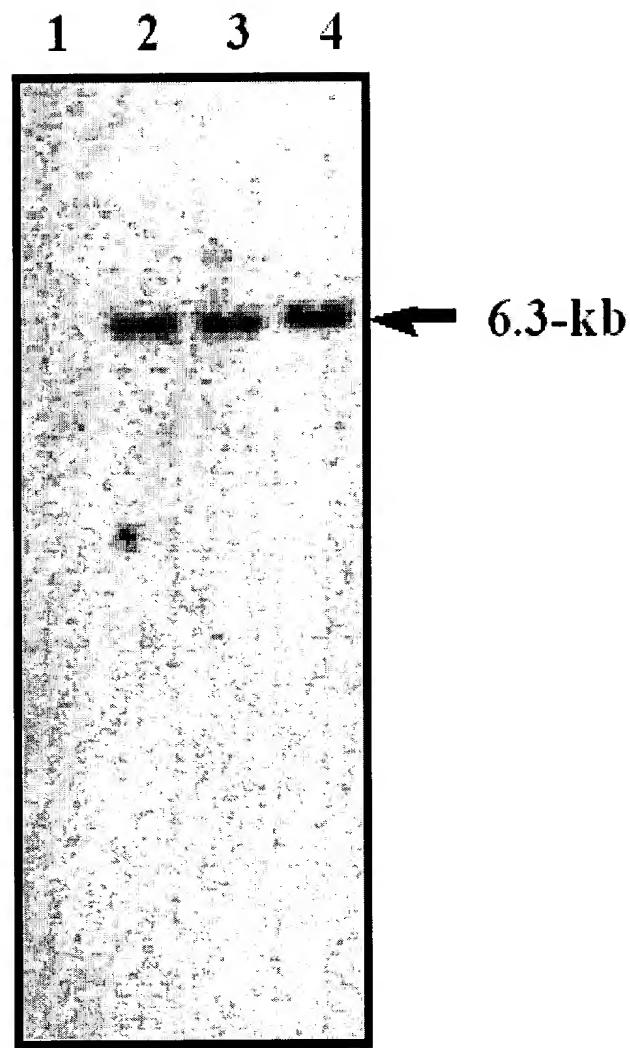


Fig. 8B

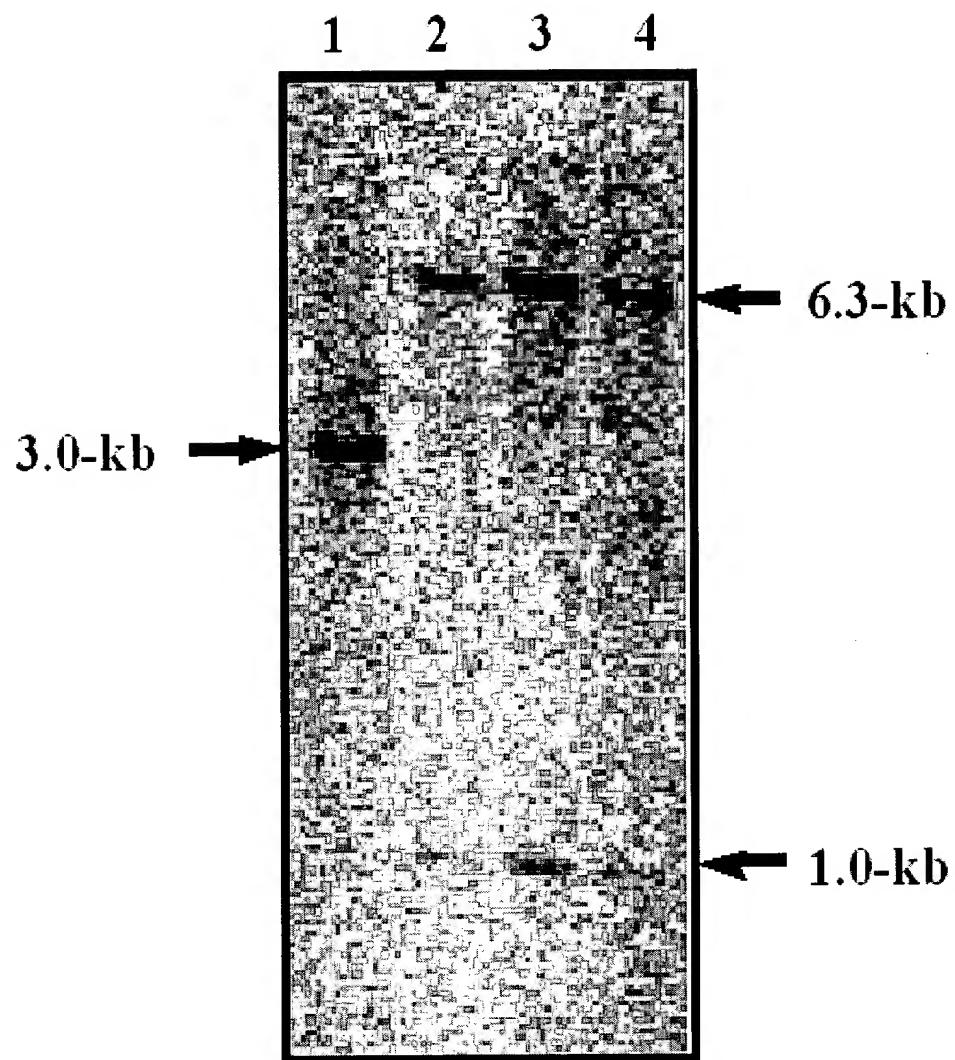


Fig. 8C

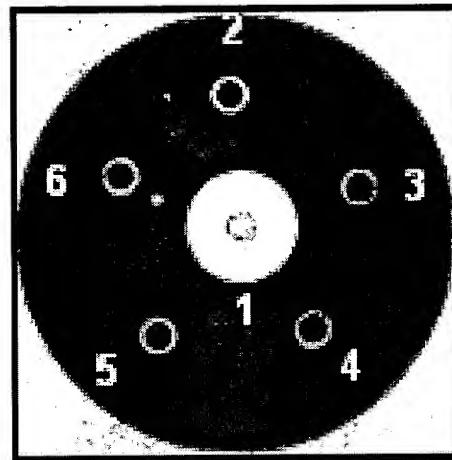


Fig. 9A

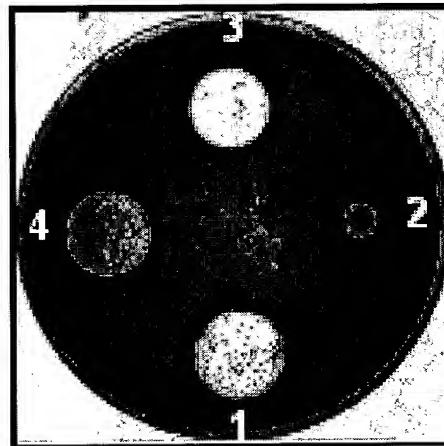


Fig. 9B

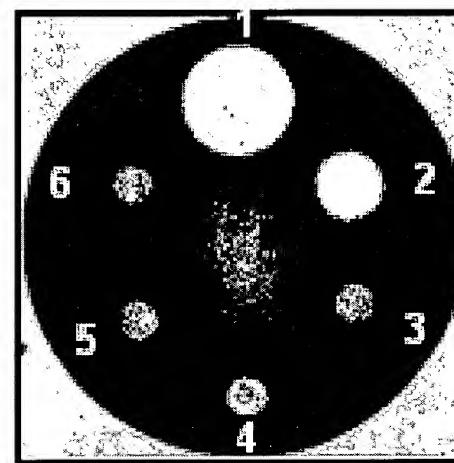


Fig. 9C

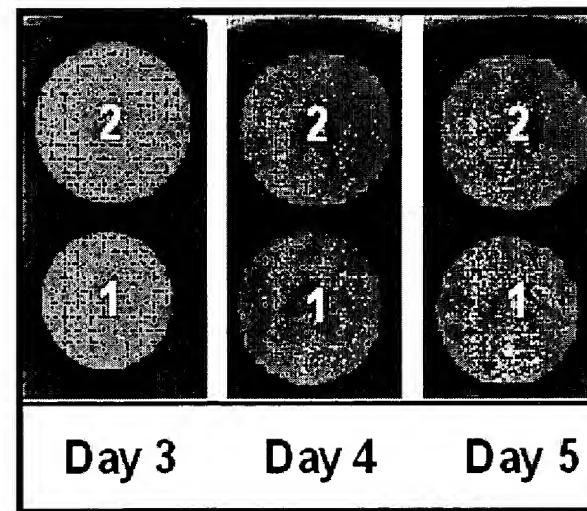


Fig. 9D

BamHI **EcorI**

| | | | |
|------|--|-------------|--------------------|
| 1 | GGATCCGGAAAGACCGGAATTCCCCCGGTCGAACACTCGTATCGCTCTGGTAGAACTGACGAAGGGTCAATCGGC | GTGAC | AAGGAGGGGGACCG 100 |
| 101 | ATGAGGATGGTGGTACGTGACTCCGGCAATCCGGCCAACTCCGGTACACTCCGGCCATCGGCGGTTACACCTTCGTC | SGCA | > |
| | SACII | | |
| 201 | CGGTCTGGACAAGGTGACTCCGGCAATCCGGCCAACTCCGGTACACTCCGGCCATCGGCGGTTACACCTTCGTC | 300 | |
| | V L D K L T Y S G N P A N L T S V A A H P R Y T F V Q G D T V D P | | |
| 301 | CGCGTCGTCGACGGTGGTCGGCCACGACGTCACTCGTCACACTCGTCACACTCGTCGACGGTGGACCGCTCGATCGACACCCGGCTCGTC | 400 | |
| | R V V D E V V A G H D V I V H F A A E S H V D R S I D T A T R F V | | |
| 401 | ACGACCAACGGTGTGGTGGAAAGGGCTCTCGGGCACGGGGCTCTCGGGCACGGGGCTCTCGGGCACGGGGCTACGGGGTCTACGGGTGGA | 500 | |
| | T T N V L G T Q T L E A A L R H G V G R F V H V S T D E V Y G S I | | |
| 501 | TCGCCCTCGGCTCATGGACCGAGGACACCCGGCTCGCCCCAACGTCGCCCTACGGGGCTCGAAGGGGGTCTGGACCTGATGGGCTCGGCACCG | 600 | |
| | A S G S W T E D T P L A P N V P Y A A S K A G S D L M A L A W H R | | |
| 601 | CACCCGGGGCTGGACCTGGTGTGCTCACCCGGTGCACCAACTACGGTCCCTACCCAGTACCGTACCCCGAGAAGGGTGTATCCCGCTCTCGTACCAACATCCTC | 700 | |
| | T R G L D V V T R C T N N Y G P Y Q Y P E K V I P L F V T N I L | | |
| 701 | GACGGCTTGGGGTGGCCCTGTACGGGGACGGGGCCACCGGGGACGGGGTGTACGGGGACTGGCTGCACTGGTGTCCGACACTGGCTCATGAACTCCG | 800 | |
| | D G L R V P L Y G D G A H R R D W L H V S D H C R A I Q M V M N S G | | |
| 801 | GCCCCGGGGAGGTCTACCAACGGAAACTCTCCAACGGAAACTCAACGGGTCTGGCTCACGGGGTGTGGCTACGGGGCACCGACTGGTCTCTG | 900 | |
| | R A G E V Y H I G G T E L S N E E L T G L L T A C G T D W S C | | |
| 901 | CGTGGACCGGGTGGCCACGGGGCACGGGGCACGGGGTGTGGACTACTCGCTCGACATCACGAAGATCCGGCAGGAACCTGGGTACAGGGCTGGCTTC | 1000 | |
| | V D R V A D R Q G H D R R Y S L D I T K I R Q E L G Y E P L V A F | | |
| 1001 | KpnI | | |
| | GAGGACGGCTTGGCCGGACGGTGAAGTGGTACACGAGAAACCGTCTGGTGGCAGCCGCTCTGGACGGCGCTGGCTGAC | 1100 | |
| | E D G L A A T V K W Y H E N R S W W Q P L K E A A G L L D A V G * | | |
| 1101 | GGCAGCCACCGCTAGGAACACCCAG GAAAG GAGGACCGTCAAGGAGCCAGTGGCTCCGGCAGGGAGTGGATCGCTCTCG 1200 | | |
| | sgcB > M T A V K E P T S R A G R R E W I A L V | | |
| 1201 | TGGTCTCTCTGGCCACGGATGCTGGTGTGATG CTGGACATCAACGTCCTCATGCTGGCCTTGCCGAGTTGAGCAGGGATCTCGGGCGGAGCACGCA | 1300 | |
| | V L S L P T M L L D I N V L M L A L P Q L S E D L G A S S T Q | | |
| 1301 | ACAGCTGTGGATCACCGACATCTACGGATTGGCATGGCTGGGATGGGACCCCTGGCGACGGGATGGCCGGCAGGGCTCTGGTCTCGTC | 1400 | |
| | Q L W I T D I Y G F A I A G F L V T M G T L G D R I G R R L L L | | |
| 1401 | GGGGGGGGCGCTTCGGGTCTCGGACGGGGATGGCTCGTCTGGCTGGCTGGGATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGGG | 1500 | |
| | G G A A V F A V V S V A F S D S A A M L V V S R A V L G V A G A | | |
| 1501 | CCACGGTGATGCCCTCGACGCTGGCTCATCGAAACATGTTGAGGACCCCAAGGAGGGGGCACCGCCATGCCATGGGGGAGGCCATGATGGC | 1600 | |
| | T V M P S T L A L I S N M F E D P K E R G T A I A M W A S A M M A | | |
| 1601 | CGAGTCGCCCTCGGGCCGGCTCGCCGGCTGGCTGGGGATCGGTCTCATGCCATGGGGGAGGCCATGATGGCTGGGGT | 1700 | |
| | G V A L G P A V G L V L A A F W W G S V F L I A V P V M L L V V | | |

Fig. 6





Fig. 6 cont'd.